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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/784,528

DATE: 08/30/2004

TIME: 14:56:52

Input Set : N:\Crf3\RULE60\10784528.raw.txt

Output Set: N:\CRF4\08302004\J784528.raw

1 <110> APPLICANT: Case Western Reserve University
 2 Brown, Arthur M.
 3 Wible, Barbara A.
 4 <120> TITLE OF INVENTION: Methods of Inducing Apoptosis in Hyperproliferative Cells
 5 <130> FILE REFERENCE: 22884/04047
 6 <140> CURRENT APPLICATION NUMBER: US/10/784,528
 7 <141> CURRENT FILING DATE: 2004-02-23
 8 <150> PRIOR APPLICATION NUMBER: US/10/000,778
 9 <151> PRIOR FILING DATE: 2001-10-31
 10 <160> NUMBER OF SEQ ID NOS: 2
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1725
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 17 <400> SEQUENCE: 1

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20	cccattcccc caacgctggt ggcccctggc accctgctgg gccccaagcg tgaggtggac	180
21	atgcaccccc ctctgccccca gctgtgcac cctgatgtca ccatgaaacc attgcccttc	240
22	tatgaagtct atggggagct catccggccc accacccttg catccacttc tagccagcgg	300
23	tttgaggaag cgcactttac ctttgccctc acaccccagc aagtgcagca gattcttaca	360
24	tccagagagg ttctgccagg agccaaatgt gattatacca tacaggtgca gctaagggtc	420
25	tgtctctgtg agaccagctg cccccaggaa gattattttc cccccaacct ctttgtcaag	480
26	gttaatggga aactgtgccc cctgcccggg taccttcccc caaccaagaa tggggccgag	540
27	cccaagaggc ccagccgccc catcaacatc acacccttg ctcgactctc agccactgtt	600
28	cccaacacca ttgtggtcaa ttggtcatct gaggtcggac ggaattactc cttgtctgtg	660
29	tacctggtga ggcagttgac tgcaggaacc cttctacaaa aactcagagc aaagggtatc	720
30	cggaaaccag accactcgcg ggcactgac aaggagaaat tgactgctga ccctgacagt	780
31	gaggtggcca ctacaagtct cggggtgtca ctcatgtgcc cgctagggaa gatgcgcctg	840
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33	ctacagatga atgagaagaa gcctacatgg acatgtcctg tgtgtgacaa gaaggctccc	960
34	tatgaatctc ttatcattga tgggtttatt atggagattc ttagttcctg ttcagattgt	1020
35	gatgagatcc aattcatgga agatggatcc tgggtgccc aa tgaaacccaa gaaggaggca	1080
36	tctgaggttt gccccccgcc aggggtatgg ctggatggcc tccagtacag cccagtccag	1140
37	gggggagatc catcagagaa taagaagaag gtcgaagtta ttgacttgac aatagaaagc	1200
38	tcatcagatg aggaggatct gccccctacc aagaagcact gttctgtcac ctcagctgcc	1260
39	atccccggcc tacctggaag caaaggagtc ctgacatctg gccaccagcc atcctcggtg	1320
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43	gcccttgccc acttcttcca gtaccgaggg accccttctc actttctggg cccactggcc	1560
44	cccacgctgg ggagctccca ctgcagcgcc actccggcgc cccctcctgg ccgtgtcagc	1620

ENTERED

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45      agcattgtgg cccctggggg ggccttgagg gaggggcatg gaggaccct gccctcaggt 1680
46      ccctctttga ctggctgtcg gtcagacatc atttcctgg actga 1725
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49 <211> LENGTH: 574
50 <212> TYPE: PRT
51 <213> ORGANISM: Homo sapiens
52 <400> SEQUENCE: 2
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56      20          25          30
57      Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala
58      35          40          45
59      Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
60      50          55          60
61      Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
62      65          70          75          80
63      Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
64      85          90          95
65      Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
66      100         105         110
67      Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
68      115         120         125
69      Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
70      130         135         140
71      Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
72      145         150         155         160
73      Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
74      165         170         175
75      Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
76      180         185         190
77      Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
78      195         200         205
79      Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
80      210         215         220
81      Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
82      225         230         235         240
83      Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
84      245         250         255
85      Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
86      260         265         270
87      Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
88      275         280         285
89      Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
90      290         295         300
91      Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
92      305         310         315         320
93      Tyr Glu Ser Leu Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser
94      325         330         335

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```

95   Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
96           340                      345                      350
97   Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Gly
98           355                      360                      365
99   Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro
100          370                      375                      380
101   Ser Glu Asn Lys Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser
102          385                      390                      395                      400
103   Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val
104           405                      410                      415
105   Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr
106           420                      425                      430
107   Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr
108           435                      440                      445
109   Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro
110          450                      455                      460
111   Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe
112          465                      470                      475                      480
113   Leu Gln Thr Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu
114           485                      490                      495
115   Asp Glu Gln Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro
116           500                      505                      510
117   Ser His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys
118           515                      520                      525
119   Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala
120          530                      535                      540
121   Pro Gly Gly Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly
122          545                      550                      555                      560
123   Pro Ser Leu Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp
124           565                      570

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

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